

#4

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/904,987

DATE: 10/18/2001

TIME: 09:47:02

Input Set : A:\ES.txt

Output Set: N:\CRF3\10182001\I904987.raw

3 <110> APPLICANT: Novactyl, Inc.
5 <120> TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepathological

6 Protein Assembly or Aggregation
8 <130> FILE REFERENCE: 42108/26146
10 <140> CURRENT APPLICATION NUMBER: 09/904,987
11 <141> CURRENT FILING DATE: 2001-07-12
13 <160> NUMBER OF SEQ ID NOS: 7
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 43
19 <212> TYPE: PRT
20 <213> ORGANISM: homo sapiens
22 <300> PUBLICATION INFORMATION:
23 <308> DATABASE ACCESSION NO: NCBI ENTREZ / QRHUA4
24 <309> DATABASE ENTRY DATE: 2000-09-15
25 <313> RELEVANT RESIDUES: (672)..(714)
27 <400> SEQUENCE: 1

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29 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
30 1 5 10 15
32 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
33 20 25 30
35 Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
36 35 40

38 <210> SEQ ID NO: 2
39 <211> LENGTH: 770
40 <212> TYPE: PRT
41 <213> ORGANISM: homo sapiens
43 <300> PUBLICATION INFORMATION:
44 <308> DATABASE ACCESSION NO: NCBI ENTREZ / QRHUA4
45 <309> DATABASE ENTRY DATE: 2000-09-15
46 <313> RELEVANT RESIDUES: (1)..(770)
48 <400> SEQUENCE: 2

50 Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
51 1 5 10 15
53 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
54 20 25 30
56 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
57 35 40 45
59 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
60 50 55 60
62 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
63 65 70 75 80
65 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
66 85 90 95
68 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
69 100 105 110
71 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu

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72          115          120          125
74 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
75          130          135          140
77 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
78 145          150          155          160
80 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
81          165          170          175
83 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
84          180          185          190
86 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
87          195          200          205
89 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
90          210          215          220
92 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
93 225          230          235          240
95 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
96          245          250          255
98 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
99          260          265          270
101 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
102          275          280          285
104 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
105          290          295          300
107 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
108 305          310          315          320
110 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
111          325          330          335
113 Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
114          340          345          350
116 Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
117          355          360          365
119 Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
120          370          375          380
122 Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
123 385          390          395          400
125 Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
126          405          410          415
128 Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
129          420          425          430
131 Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
132          435          440          445
134 Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
135          450          455          460
137 Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
138 465          470          475          480
140 Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
141          485          490          495
143 Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
144          500          505          510

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146 Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
147          515          520          525
149 Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
150          530          535          540
152 Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
153 545          550          555          560
155 Glu Val Asp Glu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
156          565          570          575
158 Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
159          580          585          590
161 Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
162          595          600          605
164 Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
165          610          615          620
167 Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
168 625          630          635          640
170 Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
171          645          650          655
173 Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
174          660          665          670
176 Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
177          675          680          685
179 Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
180          690          695          700
182 Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
183 705          710          715          720
185 Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
186          725          730          735
188 Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
189          740          745          750
191 Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
192          755          760          765
194 Gln Asn
195          770
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 253
199 <212> TYPE: PRT
200 <213> ORGANISM: homo sapiens
202 <300> PUBLICATION INFORMATION:
203 <308> DATABASE ACCESSION NO: NCBI ENTREZ / XM_009567
204 <309> DATABASE ENTRY DATE: 2001-04-17
205 <313> RELEVANT RESIDUES: (1)..(253)
207 <400> SEQUENCE: 3
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210 1          5          10          15
212 Ser Asp Leu Gly Leu Cys Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn
213          20          25          30
215 Thr Gly Gly Ser Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg
216          35          40          45

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218 Tyr Pro Pro Gln Gly Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly
219      50                      55                      60
221 Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly
222 65                      70                      75                      80
224 Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His
225                      85                      90                      95
227 Ser Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met
228                      100                     105                     110
230 Ala Gly Ala Ala Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr
231                      115                      120                      125
233 Met Leu Gly Ser Ala Met Ser Arg Pro Ile Ile His Phe Gly Ser Asp
234                      130                      135                      140
236 Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn Met His Arg Tyr Pro Asn Gln
237 145                      150                      155                      160
239 Val Tyr Tyr Arg Pro Met Asp Glu Tyr Ser Asn Gln Asn Asn Phe Val
240                      165                      170                      175
242 His Asp Cys Val Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr
243                      180                      185                      190
245 Thr Lys Gly Glu Asn Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg
246                      195                      200                      205
248 Val Val Glu Gln Met Cys Ile Thr Gln Tyr Glu Arg Glu Ser Gln Ala
249                      210                      215                      220
251 Tyr Tyr Gln Arg Gly Ser Ser Met Val Leu Phe Ser Ser Pro Pro Val
252 225                      230                      235                      240
254 Ile Leu Leu Ile Ser Phe Leu Ile Phe Leu Ile Val Gly
255                      245                      250
257 <210> SEQ ID NO: 4
258 <211> LENGTH: 140
259 <212> TYPE: PRT ,
260 <213> ORGANISM: homo sapiens
262 <300> PUBLICATION INFORMATION:
263 <308> DATABASE ACCESSION NO: NCBI ENTREZ / XM_003494
264 <309> DATABASE ENTRY DATE: 2001-04-16
265 <313> RELEVANT RESIDUES: (1)..(140)
267 <400> SEQUENCE: 4
269 Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
270 1                      5                      10                      15
272 Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
273                      20                      25                      30
275 Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
276                      35                      40                      45
278 Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
279                      50                      55                      60
281 Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
282 65                      70                      75                      80
284 Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys
285                      85                      90                      95
287 Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
288                      100                     105                     110

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290 Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro
291      115      120      125
293 Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
294      130      135      140
296 <210> SEQ ID NO: 5
297 <211> LENGTH: 758
298 <212> TYPE: PRT
299 <213> ORGANISM: homo sapiens
301 <300> PUBLICATION INFORMATION:
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303 <309> DATABASE ENTRY DATE: 2001-02-13
304 <313> RELEVANT RESIDUES: (1)..(758)
306 <400> SEQUENCE: 5
308 Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
309 1      5      10      15
311 Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
312      20      25      30
314 Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
315      35      40      45
317 Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
318      50      55      60
320 Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
321 65      70      75      80
323 Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
324      85      90      95
326 Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
327      100     105     110
329 Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Glu Pro Glu Ser
330      115     120     125
332 Gly Lys Val Val Gln Glu Gly Phe Leu Arg Glu Pro Gly Pro Pro Gly
333      130     135     140
335 Leu Ser His Gln Leu Met Ser Gly Met Pro Gly Ala Pro Leu Leu Pro
336 145     150     155     160
338 Glu Gly Pro Arg Glu Ala Thr Arg Gln Pro Ser Gly Thr Gly Pro Glu
339      165     170     175
341 Asp Thr Glu Gly Gly Arg His Ala Pro Glu Leu Leu Lys His Gln Leu
342      180     185     190
344 Leu Gly Asp Leu His Gln Glu Gly Pro Pro Leu Lys Gly Ala Gly Gly
345      195     200     205
347 Lys Glu Arg Pro Gly Ser Lys Glu Glu Val Asp Glu Asp Arg Asp Val
348      210     215     220
350 Asp Glu Ser Ser Pro Gln Asp Ser Pro Pro Ser Lys Ala Ser Pro Ala
351 225     230     235     240
353 Gln Asp Gly Arg Pro Pro Gln Thr Ala Ala Arg Glu Ala Thr Ser Ile
354      245     250     255
356 Pro Gly Phe Pro Ala Glu Gly Ala Ile Pro Leu Pro Val Asp Phe Leu
357      260     265     270
359 Ser Lys Val Ser Thr Glu Ile Pro Ala Ser Glu Pro Asp Gly Pro Ser
360      275     280     285

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VERIFICATION SUMMARY

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TIME: 09:47:03

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Output Set: N:\CRF3\10182001\I904987.raw